

Serial Number: 09/936,677

Edited by:

Verified by:

(STIC sta)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/lastname at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/936,677

DATE: 10/23/2001

TIME: 13:31:57

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10232001\I936677.raw

```

3 <110> APPLICANT: LIBON Christine
4     CORVAIA Nathalie
5     BECK Alain
6     BONNEFOY Jean-Yves
8 <120> TITLE OF INVENTION: IMMUNOSTIMULATING BACTERIAL MEMBRANE FRACTIONS IN CANCER
9     TREATMENT
11 <130> FILE REFERENCE: D17974
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/936,677
C--> 13 <141> CURRENT FILING DATE: 2001-09-14
13 <150> PRIOR APPLICATION NUMBER: FR 99 03 154
14 <151> PRIOR FILING DATE: 1999-03-15
16 <150> PRIOR APPLICATION NUMBER: PCT/FR00/00623
17 <151> PRIOR FILING DATE: 2000-03-15
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn Vers. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1035
25 <212> TYPE: DNA
26 <213> ORGANISM: Klebsiella pneumoniae
28 <220> FEATURE:
29 <221> NAME/KEY: exon
30 <222> LOCATION: (1)..(1032)
32 <220> FEATURE:
33 <221> NAME/KEY: intron
34 <222> LOCATION: (1033)..(1035)
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1)..(1032)
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41 atg aaa gca att ttc gta ctg aat gcg gct ccg aaa gat aac acc tgg 48
42 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
43 1 5 10 15
45 tat gca ggt ggt aaa ctg ggt tgg tcc cag tat cac gac acc ggt ttc 96
46 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
47 20 25 30
49 tac ggt aac ggt ttc cag aac aac aac ggt ccg acc cgt aac gat cag 144
50 Tyr Gly Asn Gly Phe Gln Asn Asn Asn Gly Pro Thr Arg Asn Asp Gln
51 35 40 45
53 ctt ggt gct ggt gcg ttc ggt ggt tac cag gtt aac ccg tac ctc ggt 192
54 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
55 50 55 60
57 ttc gaa atg ggt tat gac tgg ctg ggc cgt atg gca tat aaa ggc agc 240
58 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
59 65 70 75 80
61 gtt gac aac ggt gct ttc aaa gct cag ggc gtt cag ctg acc gct aaa 288
62 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
63 85 90 95

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65 ctg ggt tac ccg atc act gac gat ctg gac atc tac acc cgt ctg ggc 336
66 Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
67      100      105      110
69 ggc atg gtt tgg cgc gct gac tcc aaa ggc aac tac gct tct acc ggc 384
70 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
71      115      120      125
73 gtt tcc cgt agc gaa cac gac act ggc gtt tcc cca gta ttt gct ggc 432
74 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
75      130      135      140
77 ggc gta gag tgg gct gtt act cgt gac atc gct acc cgt ctg gaa tac 480
78 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
79 145      150      155      160
81 cag tgg gtt aac aac atc ggc gac gcg ggc act gtg ggt acc cgt cct 528
82 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
83      165      170      175
85 gat aac ggc atg ctg agc ctg ggc gtt tcc tac cgc ttc ggt cag gaa 576
86 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
87      180      185      190
89 gat gct gca ccg gtt gtt gct ccg gct ccg gct ccg gct ccg gaa gtg 624
90 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Ala Pro Glu Val
91      195      200      205
93 gct acc aag cac ttc acc ctg aag tct gac gtt ctg ttc aac ttc aac 672
94 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
95      210      215      220
97 aaa gct acc ctg aaa ccg gaa ggt cag cag gct ctg gat cag ctg tac 720
98 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
99 225      230      235      240
101 act cag ctg agc aac atg gat ccg aaa gac ggt tcc gct gtt gtt ctg 768
102 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
103      245      250      255
105 ggc tac acc gac cgc atc ggt tcc gaa gct tac aac cag cag ctg tct 816
106 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
107      260      265      270
109 gag aaa cgt gct cag tcc gtt gtt gac tac ctg gtt gct aaa ggc atc 864
110 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
111      275      280      285
113 ccg gct ggc aaa atc tcc gct cgc ggc atg ggt gaa tcc aac ccg gtt 912
114 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
115      290      295      300
117 act ggc aac acc tgt gac aac gtg aaa gct cgc gct gcc ctg atc gat 960
118 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
119 305      310      315      320
121 tgc ctg gct ccg gat cgt cgt gta gag atc gaa gtt aaa ggc tac aaa 1008
122 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
123      325      330      335
125 gaa gtt gta act cag ccg gcg ggt taa 1035
126 Glu Val Val Thr Gln Pro Ala Gly
127      340
130 <210> SEQ ID NO: 2

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RAW SEQUENCE LISTING

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131 <211> LENGTH: 344
132 <212> TYPE: PRT
133 <213> ORGANISM: Klebsiella pneumoniae
135 <400> SEQUENCE: 2
136 Met Lys Ala Ile Phe Val Leu Asn Ala Ala Pro Lys Asp Asn Thr Trp
137   1      5      10      15
139 Tyr Ala Gly Gly Lys Leu Gly Trp Ser Gln Tyr His Asp Thr Gly Phe
140      20      25      30
142 Tyr Gly Asn Gly Phe Gln Asn Asn Gly Pro Thr Arg Asn Asp Gln
143      35      40      45
145 Leu Gly Ala Gly Ala Phe Gly Gly Tyr Gln Val Asn Pro Tyr Leu Gly
146      50      55      60
148 Phe Glu Met Gly Tyr Asp Trp Leu Gly Arg Met Ala Tyr Lys Gly Ser
149      65      70      75      80
151 Val Asp Asn Gly Ala Phe Lys Ala Gln Gly Val Gln Leu Thr Ala Lys
152      85      90      95
154 Leu Gly Tyr Pro Ile Thr Asp Asp Leu Asp Ile Tyr Thr Arg Leu Gly
155      100     105     110
157 Gly Met Val Trp Arg Ala Asp Ser Lys Gly Asn Tyr Ala Ser Thr Gly
158      115     120     125
160 Val Ser Arg Ser Glu His Asp Thr Gly Val Ser Pro Val Phe Ala Gly
161      130     135     140
163 Gly Val Glu Trp Ala Val Thr Arg Asp Ile Ala Thr Arg Leu Glu Tyr
164 145      150     155     160
166 Gln Trp Val Asn Asn Ile Gly Asp Ala Gly Thr Val Gly Thr Arg Pro
167      165     170     175
169 Asp Asn Gly Met Leu Ser Leu Gly Val Ser Tyr Arg Phe Gly Gln Glu
170      180     185     190
172 Asp Ala Ala Pro Val Val Ala Pro Ala Pro Ala Pro Glu Val
173      195     200     205
175 Ala Thr Lys His Phe Thr Leu Lys Ser Asp Val Leu Phe Asn Phe Asn
176      210     215     220
178 Lys Ala Thr Leu Lys Pro Glu Gly Gln Gln Ala Leu Asp Gln Leu Tyr
179 225      230     235     240
181 Thr Gln Leu Ser Asn Met Asp Pro Lys Asp Gly Ser Ala Val Val Leu
182      245     250     255
184 Gly Tyr Thr Asp Arg Ile Gly Ser Glu Ala Tyr Asn Gln Gln Leu Ser
185      260     265     270
187 Glu Lys Arg Ala Gln Ser Val Val Asp Tyr Leu Val Ala Lys Gly Ile
188      275     280     285
190 Pro Ala Gly Lys Ile Ser Ala Arg Gly Met Gly Glu Ser Asn Pro Val
191      290     295     300
193 Thr Gly Asn Thr Cys Asp Asn Val Lys Ala Arg Ala Ala Leu Ile Asp
194 305      310     315     320
196 Cys Leu Ala Pro Asp Arg Arg Val Glu Ile Glu Val Lys Gly Tyr Lys
197      325     330     335
199 Glu Val Val Thr Gln Pro Ala Gly
200      340
203 <210> SEQ ID NO: 3

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RAW SEQUENCE LISTING

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10232001\I936677.raw

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204 <211> LENGTH: 303
205 <212> TYPE: DNA
206 <213> ORGANISM: Klebsiella pneumoniae
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)..(303)
212 <400> SEQUENCE: 3
213 acc gtg aaa acc aaa aac acc acg acc acc cag acc cag ccg agc aaa 48
214 Thr Val Lys Thr Lys Asn Thr Thr Thr Gln Thr Gln Pro Ser Lys
215 1 5 10 15
217 ccg acc acc aaa cag cgt cag aac aaa ccg ccg aac aaa ccg aac aac 96
218 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn
219 20 25 30
221 gat ttc cat ttc gaa gtg ttc aac ttc gtg ccg tgc agc atc tgc agc 144
222 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser
223 35 40 45
225 aac aac ccg acc tgc tgg gcg atc tgc aaa cgt atc ccg aac aaa aaa 192
226 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys
227 50 55 60
229 ccg ggc aaa aaa acc acg acc aaa ccg acc aaa aaa ccg acc ttc aaa 240
230 Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys
231 65 70 75 80
233 acc acc aaa aaa gat cat aaa ccg cag acc acc aaa ccg aaa gaa gtg 288
234 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val
235 85 90 95
237 ccg acc acc aaa ccg 303
238 Pro Thr Thr Lys Pro
239 100
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 101
244 <212> TYPE: PRT
245 <213> ORGANISM: Klebsiella pneumoniae
247 <400> SEQUENCE: 4
248 Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Thr Gln Pro Ser Lys
249 1 5 10 15
251 Pro Thr Thr Lys Gln Arg Gln Asn Lys Pro Pro Asn Lys Pro Asn Asn
252 20 25 30
254 Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys Ser
255 35 40 45
257 Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys Lys
258 50 55 60
260 Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Phe Lys
261 65 70 75 80
263 Thr Thr Lys Lys Asp His Lys Pro Gln Thr Thr Lys Pro Lys Glu Val
264 85 90 95
266 Pro Thr Thr Lys Pro
267 100

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VERIFICATION SUMMARY

DATE: 10/23/2001

PATENT APPLICATION: US/09/936,677

TIME: 13:31:58

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10232001\I936677.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date